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SEQUENCE LISTING

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Conroy, Louise A  
Tempest, Philip R

<120> Specific binding members for TGF beta 1

<130> 28111/37903

<140> To be assigned

<141> Herewith

<150> PCT/GB00/01679

<151> 2000-05-02

<150> US 60/131,983

<151> 1999-04-30

<160> 25

<170> PatentIn Ver. 2.1

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<211> 369

<212> DNA

<213> Homo sapiens

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ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtat taaatactat 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gcgaactggg 300  
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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Thr Gly Glu Tyr Ser Gly Tyr Asp Thr Ser Gly Val Glu Leu  
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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120

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ccaggcaagg agctggagtg ggtggcagtt atatcatatg atggaagtat taaatactat 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gcgaactggg 300  
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35 40 45  
Ala Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

	85		90		95
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 gggaaagccc ctatcctcct gatctatggg acatccactt taaaaagtgg ggtcccgtca 180  
 aggttcagcg gcagtggatc tggcacagat ttcactctca ccatcaacag cctgcagcct 240  
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 35 40 45  
 Tyr Gly Thr Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro  
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 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Ser Asn Tyr Pro Leu  
 85 90 95  
 Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys  
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aggttcagcg gcagtggatc tggcacagat ttcactctca ccatcaacag cctgcagcct 240  
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35 40 45  
Tyr Gly Thr Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro  
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Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Ser Asn Tyr Pro Leu  
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Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys  
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ccaggcaagg agctggagtg ggtggcagtt atatcatatg atggaagtat taaatactat 180  
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gcgaactggt 300  
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30  
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Glu Leu Glu Trp Val  
35 40 45  
Ala Val Ile Ser Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Arg Thr Gly Glu Tyr Ser Gly Tyr Asp Thr Pro Ala Ser Pro Asp  
100 105 110  
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
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<210> 11  
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<210> 12  
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<212> PRT  
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<210> 15  
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<210> 24  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
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<210> 25  
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<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
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<400> 25  
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